

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092707_us-10-553-669-1.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 121 Seconds
(without alignments)
1393.680 Million cell updates/sec

Title: US-10-553-669-1
Perfect score: 1842
Sequence: 1 MKRASAGGSRLLAWLWLQA.....TDEEPLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query			
No.	Score	Match Length	DB	ID	Description

1	1842	100.0	344	8	ADM33974	Adm33974	Human	Nog
2	1842	100.0	344	8	ADU21101	Adu21101	Human	Nog
3	1842	100.0	344	9	ADY34440	Ady34440	Human	Nog
4	1842	100.0	344	9	AEB19597	Aeb19597	Human	Nog
5	1842	100.0	344	9	AEB86619	Aeb86619	Human	NOG
6	1842	100.0	472	3	AAB33426	Aab33426	Human	PRO
7	1842	100.0	473	2	AAy41745	Aay41745	Human	PRO
8	1842	100.0	473	3	AAB44301	Aab44301	Human	PRO
9	1842	100.0	473	3	AAB24410	Aab24410	Human	PRO
10	1842	100.0	473	3	AAy95345	Aay95345	Human	PRO
11	1842	100.0	473	4	AAU12362	Aau12362	Human	PRO
12	1842	100.0	473	4	AAU04589	Aau04589	Human	Nog
13	1842	100.0	473	4	AAB49891	Aab49891	Human	PRO
14	1842	100.0	473	4	AAB50908	Aab50908	Human	PRO
15	1842	100.0	473	5	AAU83655	Aau83655	Human	PRO
16	1842	100.0	473	5	AAO21479	Aao21479	Human	NgR
17	1842	100.0	473	5	ABB81081	Abb81081	Human	Nog
18	1842	100.0	473	5	ADY31868	Ady31868	Novel	hum
19	1842	100.0	473	6	ABO17806	Ab017806	Novel	hum
20	1842	100.0	473	6	ABU80802	Abu80802	Human	PRO
21	1842	100.0	473	6	ABO25247	Abo25247	Novel	hum
22	1842	100.0	473	6	ABO33768	Abo33768	Novel	hum
23	1842	100.0	473	6	ABU81060	Abu81060	Human	PRO
24	1842	100.0	473	6	ABU72253	Abu72253	Novel	hum
25	1842	100.0	473	6	ABU66760	Abu66760	Human	PRO
26	1842	100.0	473	6	ABU84933	Abu84933	Human	sec
27	1842	100.0	473	6	ABU59841	Abu59841	Novel	sec
28	1842	100.0	473	6	ABU61131	Abu61131	Human	PRO
29	1842	100.0	473	6	ABO25031	Abo25031	Human	sec
30	1842	100.0	473	6	ABU80400	Abu80400	Human	sec
31	1842	100.0	473	6	ABU82111	Abu82111	Novel	hum
32	1842	100.0	473	6	ABU67036	Abu67036	Human	sec
33	1842	100.0	473	6	ABR59665	Abr59665	Human	Nog
34	1842	100.0	473	6	ADA45901	Ada45901	Novel	hum
35	1842	100.0	473	6	ADA76332	Ada76332	Human	PRO
36	1842	100.0	473	6	ABJ72291	Abj72291	Human	PRO
37	1842	100.0	473	6	ADA18982	Ada18982	Human	PRO
38	1842	100.0	473	6	ADA61605	Ada61605	Homo sapi	
39	1842	100.0	473	6	ADB19390	Adb19390	Novel	hum
40	1842	100.0	473	6	ADB27931	Adb27931	Human	PRO
41	1842	100.0	473	6	ADA86410	Ada86410	Novel	hum
42	1842	100.0	473	6	ADB15974	Adb15974	Human	PRO
43	1842	100.0	473	6	ADA47760	Ada47760	Human	PRO
44	1842	100.0	473	6	ADA67555	Ada67555	Human	PRO
45	1842	100.0	473	6	ADB30562	Adb30562	Human	PRO

ALIGNMENTS

RESULT 1

ADM33974

ID ADM33974 standard; protein; 344 AA.

XX

AC ADM33974;

XX

DT 03-JUN-2004 (first entry)

XX

DE Human Nogo receptor-1 1-344 amino acid sequence SEQ ID NO:6.

XX

KW immunogenic; Nogo receptor-1; neuroprotective; nootropic; anticonvulsant;

KW antiparkinsonian; cerebroprotective; vasotropic; vulnerary; gene therapy;

KW multiple sclerosis; ALS; Huntington's disease; Alzheimer's disease;

KW Parkinson's disease; diabetic neuropathy; stroke; traumatic brain injury;

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092707_us-10-553-669-2.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 121 Seconds
(without alignments)
1393.680 Million cell updates/sec

Title: US-10-553-669-2
Perfect score: 1838
Sequence: 1 MKRASSGG SRLPTWVLWLQA.....TDEELLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID Length DB	Description
------------	-------	-------------	--------------	-------------

1	1838	100.0	344	8	ADM33976	Adm33976	Rat	Nogo
2	1838	100.0	344	8	ADU21102	Adu21102	Rat	Nogo
3	1838	100.0	344	9	ADY34442	Ady34442	Rat	Nogo
4	1838	100.0	344	9	AEB19599	Aeb19599	Rat	Nogo
5	1827.5	99.4	345	9	AEB86620	Aeb86620	Rat	NOGO
6	1816	98.8	471	10	AEH43954	Aeh43954	Rat	Ngr-1
7	1793	97.6	441	8	ADT77804	Adt77804	Chimeric	
8	1793	97.6	473	8	ADT77786	Adt77786	Rat	Nogo
9	1739	94.6	473	4	AAB87102	Aab87102	Mouse	sec
10	1739	94.6	473	4	AAU04590	Aau04590	Mouse	Nog
11	1739	94.6	473	5	AAO21488	Aao21488	Mouse	NgR
12	1739	94.6	473	5	AAE26454	Aae26454	Mouse	TAN
13	1739	94.6	473	5	ABB81082	Abb81082	Mouse	Nog
14	1739	94.6	473	6	ABR59666	Abr59666	Murine	No
15	1739	94.6	473	8	ADG75447	Adg75447	Mouse	NoG
16	1739	94.6	473	9	AEB19596	Aeb19596	Soluble	N
17	1739	94.6	473	10	AEK91090	Aek91090	Mouse	TAN
18	1736	94.5	473	4	AAB87169	Aab87169	Mouse	sec
19	1736	94.5	473	4	AAB87166	Aab87166	Mouse	sec
20	1735	94.4	473	4	AAB87167	Aab87167	Mouse	sec
21	1735	94.4	473	4	AAB87168	Aab87168	Mouse	sec
22	1702	92.6	319	9	AEB19608	Aeb19608	Rat	solub
23	1695	92.2	318	8	ADU21106	Adu21106	Rat	Nogo
24	1695	92.2	318	9	AEB86602	Aeb86602	Rat	NOGO
25	1654	90.0	310	8	ADM33977	Adm33977	Rat	Nogo
26	1654	90.0	310	9	ADY34443	Ady34443	Rat	Nogo
27	1654	90.0	310	9	AEB19600	Aeb19600	Rat	Nogo
28	1635	89.0	420	8	ADT77798	Adt77798	Chimeric	
29	1635	89.0	452	8	ADT77806	Adt77806	Chimeric	
30	1612	87.7	473	8	ADG75446	Adg75446	Macaque	b
31	1611	87.6	423	4	AAB87116	Aab87116	Mouse	TAN
32	1611	87.6	447	4	AAB87104	Aab87104	Mouse	mat
33	1605	87.3	344	8	ADM33974	Adm33974	Human	Nog
34	1605	87.3	344	8	ADU21101	Adu21101	Human	Nog
35	1605	87.3	344	9	ADY34440	Ady34440	Human	Nog
36	1605	87.3	344	9	AEB19597	Aeb19597	Human	Nog
37	1605	87.3	344	9	AEB86619	Aeb86619	Human	NOG
38	1605	87.3	472	3	AAB33426	Aab33426	Human	PRO
39	1605	87.3	473	2	AAY41745	Aay41745	Human	PRO
40	1605	87.3	473	3	AAB44301	Aab44301	Human	PRO
41	1605	87.3	473	3	AAB24410	Aab24410	Human	PRO
42	1605	87.3	473	3	AAY95345	Aay95345	Human	PRO
43	1605	87.3	473	4	AAU12362	Aau12362	Human	PRO
44	1605	87.3	473	4	AAU04589	Aau04589	Human	Nog
45	1605	87.3	473	4	AAB49891	Aab49891	Human	PRO

ALIGNMENTS

RESULT 1

ADM33976

ID ADM33976 standard; protein; 344 AA.

XX

AC ADM33976;

XX

DT 03-JUN-2004 (first entry)

XX

DE Rat Nogo receptor-1 1-344 amino acid sequence SEQ ID NO:8.

XX

KW immunogenic; Nogo receptor-1; neuroprotective; nootropic; anticonvulsant;

KW antiparkinsonian; cerebroprotective; vasotropic; vulnerary; gene therapy;

KW multiple sclerosis; ALS; Huntington's disease; Alzheimer's disease;

KW Parkinson's disease; diabetic neuropathy; stroke; traumatic brain injury;

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 100 Seconds
(without alignments)
1393.680 Million cell updates/sec

Title: US-10-553-669-3
Perfect score: 1515
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....QRLAGRDLKRLAANDLQGCA 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
------------	-------	-------	--------------	-------	-------------

1	1515	100.0	285	8	ADU21103	Adu21103	Human	Nog
2	1515	100.0	285	9	AEB19607	Aeb19607	Human	sol
3	1515	100.0	285	9	AEB86599	Aeb86599	Human	NOG
4	1515	100.0	310	8	ADM33975	Adm33975	Human	Nog
5	1515	100.0	310	9	ADY34441	Ady34441	Human	Nog
6	1515	100.0	310	9	AEB19598	Aeb19598	Human	Nog
7	1515	100.0	319	8	ADU21104	Adu21104	Human	Nog
8	1515	100.0	319	9	AEB19606	Aeb19606	Human	sol
9	1515	100.0	319	9	AEB86600	Aeb86600	Human	NOG
10	1515	100.0	344	8	ADM33974	Adm33974	Human	Nog
11	1515	100.0	344	8	ADU21101	Adu21101	Human	Nog
12	1515	100.0	344	9	ADY34440	Ady34440	Human	Nog
13	1515	100.0	344	9	AEB19597	Aeb19597	Human	Nog
14	1515	100.0	344	9	AEB86619	Aeb86619	Human	NOG
15	1515	100.0	472	3	AAB33426	Aab33426	Human	PRO
16	1515	100.0	473	2	AAY41745	Aay41745	Human	PRO
17	1515	100.0	473	3	AAB44301	Aab44301	Human	PRO
18	1515	100.0	473	3	AAB24410	Aab24410	Human	PRO
19	1515	100.0	473	3	AAY95345	Aay95345	Human	PRO
20	1515	100.0	473	4	AAU12362	Aau12362	Human	PRO
21	1515	100.0	473	4	AAU04589	Aau04589	Human	Nog
22	1515	100.0	473	4	AAB49891	Aab49891	Human	PRO
23	1515	100.0	473	4	AAB50908	Aab50908	Human	PRO
24	1515	100.0	473	5	AAU83655	Aau83655	Human	PRO
25	1515	100.0	473	5	AAO21479	Aao21479	Human	NgR
26	1515	100.0	473	5	ABB81081	Abb81081	Human	Nog
27	1515	100.0	473	5	ADY31868	Ady31868	Novel	hum
28	1515	100.0	473	6	ABO17806	Abo17806	Novel	hum
29	1515	100.0	473	6	ABU80802	Abu80802	Human	PRO
30	1515	100.0	473	6	ABO25247	Abo25247	Novel	hum
31	1515	100.0	473	6	ABO33768	Abo33768	Novel	hum
32	1515	100.0	473	6	ABU81060	Abu81060	Human	PRO
33	1515	100.0	473	6	ABU72253	Abu72253	Novel	hum
34	1515	100.0	473	6	ABU66760	Abu66760	Human	PRO
35	1515	100.0	473	6	ABU84933	Abu84933	Human	sec
36	1515	100.0	473	6	ABU59841	Abu59841	Novel	sec
37	1515	100.0	473	6	ABU61131	Abu61131	Human	PRO
38	1515	100.0	473	6	ABO25031	Abo25031	Human	sec
39	1515	100.0	473	6	ABU80400	Abu80400	Human	sec
40	1515	100.0	473	6	ABU82111	Abu82111	Novel	hum
41	1515	100.0	473	6	ABU67036	Abu67036	Human	sec
42	1515	100.0	473	6	ABR59665	Abr59665	Human	Nog
43	1515	100.0	473	6	ADA45901	Ada45901	Novel	hum
44	1515	100.0	473	6	ADA76332	Ada76332	Human	PRO
45	1515	100.0	473	6	ABJ72291	Abj72291	Human	PRO

ALIGNMENTS

RESULT 1
ADU21103

ID ADU21103 standard; protein; 285 AA.
 XX
 AC ADU21103;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Human Nogo receptor NgR1 polypeptide fragment (residues 26-310).
 XX
 KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;
 KW neuroprotective; vaccine; gene therapy; human.
 XX
 OS Homo sapiens.

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092707_us-10-553-669-4.rag.

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DM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 112 Seconds
(without alignments)
1393.680 Million cell updates/sec

Title: US-10-553-669-4
Perfect score: 1711
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....TDEEPLGLPKCCQPDAAADKA 319

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query			
No.	Score	Match Length	DB	ID	Description

1	1711	100.0	319	8	ADU21104	Adu21104	Human	Nog
2	1711	100.0	319	9	AEB19606	Aeb19606	Human	sol
3	1711	100.0	319	9	AEB86600	Aeb86600	Human	NOG
4	1711	100.0	344	8	ADM33974	Adm33974	Human	Nog
5	1711	100.0	344	8	ADU21101	Adu21101	Human	Nog
6	1711	100.0	344	9	ADY34440	Ady34440	Human	Nog
7	1711	100.0	344	9	AEB19597	Aeb19597	Human	Nog
8	1711	100.0	344	9	AEB86619	Aeb86619	Human	NOG
9	1711	100.0	472	3	AAB33426	Aab33426	Human	PRO
10	1711	100.0	473	2	AAY41745	Aay41745	Human	PRO
11	1711	100.0	473	3	AAB44301	Aab44301	Human	PRO
12	1711	100.0	473	3	AAB24410	Aab24410	Human	PRO
13	1711	100.0	473	3	AAY95345	Aay95345	Human	PRO
14	1711	100.0	473	4	AAU12362	Aau12362	Human	PRO
15	1711	100.0	473	4	AAU04589	Aau04589	Human	Nog
16	1711	100.0	473	4	AAB49891	Aab49891	Human	PRO
17	1711	100.0	473	4	AAB50908	Aab50908	Human	PRO
18	1711	100.0	473	5	AAU83655	Aau83655	Human	PRO
19	1711	100.0	473	5	AAO21479	Aao21479	Human	NgR
20	1711	100.0	473	5	ABB81081	Abb81081	Human	Nog
21	1711	100.0	473	5	ADY31868	Ady31868	Novel	hum
22	1711	100.0	473	6	ABO17806	Abo17806	Novel	hum
23	1711	100.0	473	6	ABU80802	Abu80802	Human	PRO
24	1711	100.0	473	6	ABO25247	Abo25247	Novel	hum
25	1711	100.0	473	6	ABO33768	Abo33768	Novel	hum
26	1711	100.0	473	6	ABU81060	Abu81060	Human	PRO
27	1711	100.0	473	6	ABU72253	Abu72253	Novel	hum
28	1711	100.0	473	6	ABU66760	Abu66760	Human	PRO
29	1711	100.0	473	6	ABU84933	Abu84933	Human	sec
30	1711	100.0	473	6	ABU59841	Abu59841	Novel	sec
31	1711	100.0	473	6	ABU61131	Abu61131	Human	PRO
32	1711	100.0	473	6	ABO25031	Abo25031	Human	sec
33	1711	100.0	473	6	ABU80400	Abu80400	Human	sec
34	1711	100.0	473	6	ABU82111	Abu82111	Novel	hum
35	1711	100.0	473	6	ABU67036	Abu67036	Human	sec
36	1711	100.0	473	6	ABR59665	Abr59665	Human	Nog
37	1711	100.0	473	6	ADA45901	Ada45901	Novel	hum
38	1711	100.0	473	6	ADA76332	Ada76332	Human	PRO
39	1711	100.0	473	6	ABJ72291	Abj72291	Human	PRO
40	1711	100.0	473	6	ADA18982	Ada18982	Human	PRO
41	1711	100.0	473	6	ADA61605	Ada61605	Homo sapi	
42	1711	100.0	473	6	ADB19390	Adb19390	Novel	hum
43	1711	100.0	473	6	ADB27931	Adb27931	Human	PRO
44	1711	100.0	473	6	ADA86410	Ada86410	Novel	hum
45	1711	100.0	473	6	ADB15974	Adb15974	Human	PRO

ALIGNMENTS

RESULT 1
ADU21104

ID ADU21104 standard; protein; 319 AA.

XX

AC ADU21104;

XX

DT 27-JAN-2005 (first entry)

XX

DE Human Nogo receptor NgR1 polypeptide fragment (residues 26-344).

XX

KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;
KW neuroprotective; vaccine; gene therapy; human.

XX

OS Homo sapiens.

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092707_us-10-553-669-5.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 100 Seconds
(without alignments)
1393.680 Million cell updates/sec

Title: US-10-553-669-5
Perfect score: 1511
Sequence: 1 CPGACVCYNPKVTTSRPQQ.....QRLAGRDLKRLATSDLEGCA 284

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
------------	-------	---------	--------------	-------	-------------

1	1511	100.0	284	8	ADU21105	Adu21105	Rat	Nogo
2	1511	100.0	284	9	AEB19609	Aeb19609	Rat	solub
3	1511	100.0	284	9	AEB86601	Aeb86601	Rat	NOGO
4	1511	100.0	310	8	ADM33977	Adm33977	Rat	Nogo
5	1511	100.0	310	9	ADY34443	Ady34443	Rat	Nogo
6	1511	100.0	310	9	AEB19600	Aeb19600	Rat	Nogo
7	1511	100.0	318	8	ADU21106	Adu21106	Rat	Nogo
8	1511	100.0	318	9	AEB86602	Aeb86602	Rat	NOGO
9	1511	100.0	319	9	AEB19608	Aeb19608	Rat	solub
10	1511	100.0	344	8	ADM33976	Adm33976	Rat	Nogo
11	1511	100.0	344	8	ADU21102	Adu21102	Rat	Nogo
12	1511	100.0	344	9	ADY34442	Ady34442	Rat	Nogo
13	1511	100.0	344	9	AEB19599	Aeb19599	Rat	Nogo
14	1511	100.0	345	9	AEB86620	Aeb86620	Rat	NOGO
15	1489	98.5	471	10	AEH43954	Aeh43954	Rat	Ngr-1
16	1481	98.0	420	8	ADT77798	Adt77798	Chimeric	
17	1481	98.0	441	8	ADT77804	Adt77804	Chimeric	
18	1481	98.0	452	8	ADT77806	Adt77806	Chimeric	
19	1481	98.0	473	8	ADT77786	Adt77786	Rat	Nogo
20	1444	95.6	423	4	AAB87116	Aab87116	Mouse	TAN
21	1444	95.6	447	4	AAB87104	Aab87104	Mouse	mat
22	1444	95.6	473	4	AAB87167	Aab87167	Mouse	sec
23	1444	95.6	473	4	AAB87166	Aab87166	Mouse	sec
24	1444	95.6	473	4	AAB87102	Aab87102	Mouse	sec
25	1444	95.6	473	4	AAU04590	Aau04590	Mouse	Nog
26	1444	95.6	473	5	AAO21488	Aao21488	Mouse	NgR
27	1444	95.6	473	5	AAE26454	Aae26454	Mouse	TAN
28	1444	95.6	473	5	ABB81082	Abb81082	Mouse	Nog
29	1444	95.6	473	6	ABR59666	Abr59666	Murine	No
30	1444	95.6	473	8	ADG75447	Adg75447	Mouse	NoG
31	1444	95.6	473	9	AEB19596	Aeb19596	Soluble	N
32	1444	95.6	473	10	AEK91090	Aek91090	Mouse	TAN
33	1441	95.4	473	4	AAB87169	Aab87169	Mouse	sec
34	1440	95.3	473	4	AAB87168	Aab87168	Mouse	sec
35	1352	89.5	473	8	ADG75446	Adg75446	Macaque	b
36	1351	89.4	285	8	ADU21103	Adu21103	Human	Nog
37	1351	89.4	285	9	AEB19607	Aeb19607	Human	sol
38	1351	89.4	285	9	AEB86599	Aeb86599	Human	NOG
39	1351	89.4	310	8	ADM33975	Adm33975	Human	Nog
40	1351	89.4	310	9	ADY34441	Ady34441	Human	Nog
41	1351	89.4	310	9	AEB19598	Aeb19598	Human	Nog
42	1351	89.4	319	8	ADU21104	Adu21104	Human	Nog
43	1351	89.4	319	9	AEB19606	Aeb19606	Human	sol
44	1351	89.4	319	9	AEB86600	Aeb86600	Human	NOG
45	1351	89.4	344	8	ADM33974	Adm33974	Human	Nog

ALIGNMENTS

RESULT 1
ADU21105

ID ADU21105 standard; protein; 284 AA.

XX

AC ADU21105;

XX

DT 27-JAN-2005 (first entry)

XX

DE Rat Nogo receptor NgR1 polypeptide fragment (residues 27-310).

XX

KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;
KW neuroprotective; vaccine; gene therapy; rat.

XX

OS Rattus sp.

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092707_us-10-553-669-6.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 112 Seconds
(without alignments)
1393.680 Million cell updates/sec

Title: US-10-553-669-6
Perfect score: 1695
Sequence: 1 CPGACVCYNEPKVTTSRPQQ.....TDEELLGLPKCCQPDAAADKA 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
------------	-------	-------	--------------	-------	-------------

1	1695	100.0	318	8	ADU21106	Adu21106	Rat	Nogo
2	1695	100.0	318	9	AEB86602	Aeb86602	Rat	NOGO
3	1695	100.0	319	9	AEB19608	Aeb19608	Rat	solub
4	1695	100.0	344	8	ADM33976	Adm33976	Rat	Nogo
5	1695	100.0	344	8	ADU21102	Adu21102	Rat	Nogo
6	1695	100.0	344	9	ADY34442	Ady34442	Rat	Nogo
7	1695	100.0	344	9	AEB19599	Aeb19599	Rat	Nogo
8	1695	100.0	345	9	AEB86620	Aeb86620	Rat	NOGO
9	1673	98.7	471	10	AEH43954	Aeh43954	Rat	Ngr-1
10	1665	98.2	441	8	ADT77804	Adt77804	Chimeric	
11	1665	98.2	473	8	ADT77786	Adt77786	Rat	Nogo
12	1611	95.0	423	4	AAB87116	Aab87116	Mouse	TAN
13	1611	95.0	447	4	AAB87104	Aab87104	Mouse	mat
14	1611	95.0	473	4	AAB87167	Aab87167	Mouse	sec
15	1611	95.0	473	4	AAB87166	Aab87166	Mouse	sec
16	1611	95.0	473	4	AAB87102	Aab87102	Mouse	sec
17	1611	95.0	473	4	AAU04590	Aau04590	Mouse	Nog
18	1611	95.0	473	5	AAO21488	Aao21488	Mouse	NgR
19	1611	95.0	473	5	AAE26454	Aae26454	Mouse	TAN
20	1611	95.0	473	5	ABB81082	Abb81082	Mouse	Nog
21	1611	95.0	473	6	ABR59666	Abr59666	Murine	No
22	1611	95.0	473	8	ADG75447	Adg75447	Mouse	NOG
23	1611	95.0	473	9	AEB19596	Aeb19596	Soluble	N
24	1611	95.0	473	10	AEK91090	Aek91090	Mouse	TAN
25	1608	94.9	473	4	AAB87169	Aab87169	Mouse	sec
26	1607	94.8	473	4	AAB87168	Aab87168	Mouse	sec
27	1511	89.1	284	8	ADU21105	Adu21105	Rat	Nogo
28	1511	89.1	284	9	AEB19609	Aeb19609	Rat	solub
29	1511	89.1	284	9	AEB86601	Aeb86601	Rat	NOGO
30	1511	89.1	310	8	ADM33977	Adm33977	Rat	Nogo
31	1511	89.1	310	9	ADY34443	Ady34443	Rat	Nogo
32	1511	89.1	310	9	AEB19600	Aeb19600	Rat	Nogo
33	1507	88.9	420	8	ADT77798	Adt77798	Chimeric	
34	1507	88.9	452	8	ADT77806	Adt77806	Chimeric	
35	1492	88.0	473	8	ADG75446	Adg75446	Macaque	b
36	1489	87.8	319	8	ADU21104	Adu21104	Human	Nog
37	1489	87.8	319	9	AEB19606	Aeb19606	Human	sol
38	1489	87.8	319	9	AEB86600	Aeb86600	Human	NOG
39	1489	87.8	344	8	ADM33974	Adm33974	Human	Nog
40	1489	87.8	344	8	ADU21101	Adu21101	Human	Nog
41	1489	87.8	344	9	ADY34440	Ady34440	Human	Nog
42	1489	87.8	344	9	AEB19597	Aeb19597	Human	Nog
43	1489	87.8	344	9	AEB86619	Aeb86619	Human	NOG
44	1489	87.8	472	3	AAB33426	Aab33426	Human	PRO
45	1489	87.8	473	2	AAY41745	Aay41745	Human	PRO

ALIGNMENTS

RESULT 1

ADU21106

ID ADU21106 standard; protein; 318 AA.

XX

AC ADU21106;

XX

DT 27-JAN-2005 (first entry)

XX

DE Rat Nogo receptor NgR1 polypeptide fragment (residues 27-344).

XX

KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;
KW neuroprotective; vaccine; gene therapy; rat.

XX

OS Rattus sp.

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092710_us-10-553-669-1.rup.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 161 Seconds
(without alignments)
2284.144 Million cell updates/sec

Title: US-10-553-669-1
Perfect score: 1842
Sequence: 1 MKRASAGGSRLLAWLWLQA.....TDEEPLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1842	100.0	473	1 RTN4R_HUMAN	Q9bZR6 homo sapien
2	1797	97.6	473	1 RTN4R_MACFA	Q9n0E3 macaca fasc
3	1651	89.6	473	1 RTN4R_MOUSE	Q99PI8 mus musculu
4	1649	89.5	473	1 RTN4R_RAT	Q99M75 rattus norv
5	962.5	52.3	479	2 Q6DH76_BRARE	Q6dh76 brachydanio
6	959.5	52.1	479	2 Q6X3Y5_BRARE	Q6x3y5 brachydanio
7	785.5	42.6	420	1 R4RL2_HUMAN	Q86un3 homo sapien
8	785.5	42.6	420	2 Q17RL9_HUMAN	Q17rl9 homo sapien

9	778.5	42.3	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
10	776	42.1	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
11	775.5	42.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
12	775.5	42.1	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
13	773	42.0	420	1	R4RL2_RAT	Q80wd1 rattus norv
14	772	41.9	441	1	R4RL1_HUMAN	Q86un2 homo sapien
15	760	41.3	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu
16	756	41.0	445	1	R4RL1_RAT	Q80wd0 rattus norv
17	749.5	40.7	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
18	720.5	39.1	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
19	716	38.9	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
20	691.5	37.5	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
21	382	20.7	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
22	382	20.7	778	2	Q6NUI6_HUMAN	Q6nui6 homo sapien
23	381	20.7	466	2	Q66IW3_XENLA	Q66iw3 xenopus lae
24	376	20.4	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
25	375.5	20.4	481	1	NYX_HUMAN	Q9gzu5 homo sapien
26	375.5	20.4	481	2	Q2M1S4_HUMAN	Q2m1s4 homo sapien
27	372.5	20.2	453	2	Q86XY1_HUMAN	Q86xy1 homo sapien
28	371	20.1	692	2	Q4G0S0_HUMAN	Q4g0s0 homo sapien
29	369	20.0	1461	2	Q5VW18_HUMAN	Q5vw18 homo sapien
30	369	20.0	1534	1	SLIT1_HUMAN	Q75093 homo sapien
31	369	20.0	1534	2	Q5VW17_HUMAN	Q5vw17 homo sapien
32	368.5	20.0	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon
33	367	19.9	1531	1	SLIT1_RAT	Q88279 rattus norv
34	364	19.8	1531	1	SLIT1_MOUSE	Q80tr4 mus musculu
35	362	19.7	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
36	356.5	19.4	513	1	LRC24_HUMAN	Q50lg9 homo sapien
37	356	19.3	652	2	Q45R42_RAT	Q45r42 rattus norv
38	354	19.2	339	2	Q4SU68_TETNG	Q4su68 tetraodon n
39	354	19.2	652	1	LRRC4_MOUSE	Q99ph1 mus musculu
40	354	19.2	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
41	354	19.2	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
42	351	19.1	597	2	Q3I0Y3_BOVIN	Q3i0y3 bos taurus
43	351	19.1	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
44	351	19.1	606	2	Q1KS52_PIG	Q1ks52 sus scrofa
45	351	19.1	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien

ALIGNMENTS

RESULT 1

RTN4R_HUMAN

ID RTN4R_HUMAN STANDARD; PRT; 473 AA.
AC Q9BZR6;
DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2001, sequence version 1.
DT 27-JUN-2006, entry version 54.
DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66
DE receptor).
GN Name=RTN4R; Synonyms=NOGOR; ORFNames=UNQ330/PRO526;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
RA Fournier A.E., GrandPre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration."
RL Nature 409:341-346(2001).

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092710_us-10-553-669-2.rup.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 161 Seconds
(without alignments)
2284.144 Million cell updates/sec

Title: US-10-553-669-2
Perfect score: 1838
Sequence: 1 MKRASSGG SRLPTWVLWLQA.....TDEELLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1793	97.6	473	1 RTN4R_RAT	Q99m75 rattus norv
2	1739	94.6	473	1 RTN4R_MOUSE	Q99pi8 mus musculu
3	1612	87.7	473	1 RTN4R_MACFA	Q9n0e3 macaca fasc
4	1605	87.3	473	1 RTN4R_HUMAN	Q9bZR6 homo sapien
5	956.5	52.0	479	2 Q6DH76_BRARE	Q6dh76 brachydanio
6	953.5	51.9	479	2 Q6X3Y5_BRARE	Q6x3y5 brachydanio
7	747	40.6	457	2 Q6WZD1_BRARE	Q6wzd1 brachydanio
8	745.5	40.6	420	1 R4RL2_HUMAN	Q86un3 homo sapien

9	745.5	40.6	420	2	Q17RL9_HUMAN	Q17rl9 homo sapien
10	737.5	40.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
11	737	40.1	441	1	R4RL1_HUMAN	Q86un2 homo sapien
12	732.5	39.9	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
13	730	39.7	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu
14	729.5	39.7	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
15	724.5	39.4	420	1	R4RL2_RAT	Q80wd1 rattus norv
16	724	39.4	445	1	R4RL1_RAT	Q80wd0 rattus norv
17	714.5	38.9	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
18	692	37.6	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
19	685	37.3	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
20	649.5	35.3	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
21	372.5	20.3	652	2	Q45R42_RAT	Q45r42 rattus norv
22	370	20.1	1461	2	Q5VW18_HUMAN	Q5vw18 homo sapien
23	370	20.1	1534	1	SLIT1_HUMAN	O75093 homo sapien
24	370	20.1	1534	2	Q5VW17_HUMAN	Q5vw17 homo sapien
25	369	20.1	1531	1	SLIT1_RAT	O88279 rattus norv
26	367.5	20.0	652	1	LRRC4_MOUSE	Q99ph1 mus musculu
27	366	19.9	1531	1	SLIT1_MOUSE	Q80tr4 mus musculu
28	365	19.9	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
29	365	19.9	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
30	365	19.9	778	2	Q6NUI6_HUMAN	Q6nui6 homo sapien
31	364	19.8	597	2	Q3I0Y3_BOVIN	Q3i0y3 bos taurus
32	364	19.8	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
33	362	19.7	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
34	359	19.5	1529	2	Q7ZXI2_XENLA	Q7zxi2 xenopus lae
35	357	19.4	692	2	Q4G0S0_HUMAN	Q4g0s0 homo sapien
36	357	19.4	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
37	356	19.4	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
38	355	19.3	466	2	Q66IW3_XENLA	Q66iw3 xenopus lae
39	353	19.2	709	1	LRC4B_MOUSE	P0c192 mus musculu
40	349	19.0	713	1	LRC4B_HUMAN	Q9nt99 homo sapien
41	347	18.9	481	1	NYX_HUMAN	Q9gzu5 homo sapien
42	347	18.9	481	2	Q2M1S4_HUMAN	Q2m1s4 homo sapien
43	344.5	18.7	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon
44	339.5	18.5	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien
45	337.5	18.4	640	1	NGL1_HUMAN	Q9hcj2 homo sapien

ALIGNMENTS

RESULT 1

RTN4R_RAT

ID RTN4R_RAT STANDARD; PRT; 473 AA.
AC Q99M75;
DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT 10-MAY-2005, sequence version 2.
DT 27-JUN-2006, entry version 41.
DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66
DE receptor).
GN Name=Rtn4r; Synonyms=Nogor;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RA Jin W.-L., Jia W., Long M., Ju G.;
RT "Identification and preparation of polyclonal antibody against rat
RT Nogo receptor."
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]

SCORE Search Results Details for Application 10553669 and Search Result 20071121_092710_us-10-553-669-3.rup.

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This page gives you Search Results detail for the Application 10553669 and Search Result 20071121_092710_us-10-553-669-3.rup.

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3M protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 134 Seconds
(without alignments)
2284.144 Million cell updates/sec

Title: US-10-553-669-3
Perfect score: 1515
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....QRLAGRDLKRLAANDLQGCA 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1515	100.0	473	1	RTN4R_HUMAN	Q9bze6 homo sapien
2	1493	98.5	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
3	1395	92.1	473	1	RTN4R_MOUSE	Q99pi8 mus musculu
4	1391	91.8	473	1	RTN4R_RAT	Q99m75 rattus norv
5	910	60.1	479	2	Q6DH76_BRARE	Q6dh76 brachydanio
6	910	60.1	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio
7	774.5	51.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
8	773.5	51.1	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio

9	771.5	50.9	420	1	R4RL2_MOUSE	Q7m6z0	mus musculu
10	770.5	50.9	420	1	R4RL2_HUMAN	Q86un3	homo sapien
11	770.5	50.9	420	2	Q17RL9_HUMAN	Q17rl9	homo sapien
12	768.5	50.7	420	1	R4RL2_RAT	Q80wd1	rattus norv
13	761.5	50.3	441	1	R4RL1_HUMAN	Q86un2	homo sapien
14	755.5	49.9	457	2	Q6WZD1_BRARE	Q6wzd1	brachydanio
15	749.5	49.5	310	2	Q4RRQ4_TETNG	Q4rrq4	tetraodon n
16	748.5	49.4	445	1	R4RL1_MOUSE	Q8k0s5	mus musculu
17	745.5	49.2	445	1	R4RL1_RAT	Q80wd0	rattus norv
18	705	46.5	324	2	Q4S3K9_TETNG	Q4s3k9	tetraodon n
19	691.5	45.6	411	2	Q4S6L6_TETNG	Q4s6l6	tetraodon n
20	672.5	44.4	458	2	Q6WZD3_BRARE	Q6wzd3	brachydanio
21	373	24.6	466	2	Q66IW3_XENLA	Q66iw3	xenopus lae
22	372	24.6	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
23	371.5	24.5	762	2	Q5JY13_HUMAN	Q5jy13	homo sapien
24	371.5	24.5	778	2	Q6NUI6_HUMAN	Q6nui6	homo sapien
25	364.5	24.1	692	2	Q4G0S0_HUMAN	Q4g0s0	homo sapien
26	362.5	23.9	481	1	NYX_HUMAN	Q9gzu5	homo sapien
27	362.5	23.9	481	2	Q2MLS4_HUMAN	Q2mls4	homo sapien
28	358.5	23.7	453	2	Q86XY1_HUMAN	Q86xy1	homo sapien
29	354	23.4	935	2	Q4SBT7_TETNG	Q4sbt7	tetraodon n
30	352	23.2	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
31	352	23.2	417	2	Q6E4J7_PETMA	Q6e4j7	petromyzon
32	351.5	23.2	652	2	Q45R42_RAT	Q45r42	rattus norv
33	351	23.2	606	2	Q1KS52_PIG	Q1ks52	sus scrofa
34	349.5	23.1	476	1	NYX_MOUSE	P83503	mus musculu
35	349.5	23.1	652	1	LRRC4_MOUSE	Q99ph1	mus musculu
36	349.5	23.1	653	1	LRRC4_HUMAN	Q9hbw1	homo sapien
37	346.5	22.9	597	2	Q3I0Y3_BOVIN	Q3i0y3	bos taurus
38	346.5	22.9	602	2	Q58CS0_BOVIN	Q58cs0	bos taurus
39	345.5	22.8	640	2	Q4JIW0_HUMAN	Q4jiw0	homo sapien
40	343.5	22.7	605	2	Q8TAY0_HUMAN	Q8tay0	homo sapien
41	343.5	22.7	640	1	NGL1_HUMAN	Q9hcj2	homo sapien
42	343.5	22.7	640	1	NGL1_MOUSE	Q8c031	mus musculu
43	343.5	22.7	640	2	Q505E5_MOUSE	Q505e5	mus musculu
44	342.5	22.6	605	1	ALS_HUMAN	P35858	homo sapien
45	341.5	22.5	368	2	Q32QP3_EPTST	Q32qp3	eptatretus

ALIGNMENTS

RESULT 1

RTN4R_HUMAN

ID RTN4R_HUMAN STANDARD; PRT; 473 AA.
AC Q9BZR6;
DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2001, sequence version 1.
DT 27-JUN-2006, entry version 54.
DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66
DE receptor).
GN Name=RTN4R; Synonyms=NOGOR; ORFNames=UNQ330/PRO526;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
RA Fournier A.E., GrandPre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration."
RL Nature 409:341-346 (2001).